

Looping back to leap forward: transcription enters a new era.

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Public Summary:

Comparative genome analyses reveal that organismal complexity scales not with gene number but with gene regulation. The human genome likely contains hundreds of thousands of enhancers (gene regulatory sequences), with a typical protein coding region embedded in a milieu of tens of enhancers. Here we review progress in unraveling one of the outstanding mysteries of modern biology: the dynamic communication of remote enhancers with target promoters in the specification of cellular identity.

Scientific Abstract:

Comparative genome analyses reveal that organismal complexity scales not with gene number but with gene regulation. Recent efforts indicate that the human genome likely contains hundreds of thousands of enhancers, with a typical gene embedded in a milieu of tens of enhancers. Proliferation of cis-regulatory DNAs is accompanied by increased complexity and functional diversification of transcriptional machineries recognizing distal enhancers and core promoters and by the high-order spatial organization of genetic elements. We review progress in unraveling one of the outstanding mysteries of modern biology: the dynamic communication of remote enhancers with target promoters in the specification of cellular identity.

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